

SEQUENCE LISTING

<110> Deutsches Krebsforschungszentrum

<120> Use of ADAM 12 for diagnosis and therapy of preeclampsia

<130> DK62208PC

<150> EP03023815.8

<151> 2003-10-17

<160> 20

<170> PatentIn version 3.1

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<213> Homo sapiens

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<221> CDS

<222> (307)..(3036)

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cgcgagggct 180

ccggagctga ctcgcccagg cagggaaatcc ctccggtcgc gacgccccgc
 cccgctcggc 240

gcccgcgtgg gatgggtgcag cgctcgccgc cggggcccgag agctgctgca
 ctgaaggccg 300

gcgacg atg gca gcg cgc ccg ctg ccc gtg tcc ccc gcc cgc gcc ctc
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Met	Ala	Ala	Arg	Pro	Leu	Pro	Val	Ser	Pro	Ala	Arg	Ala	Leu
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Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	Ser
				35					40				45		

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 492

Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	Ser	Lys
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 540

Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	Ser	Lys	Glu
				65				70				75			

ctg atc ata aat ctg gaa aga aat gaa ggt ctc att gcc agc agt ttc
 588

Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	Ala	Ser	Ser	Phe
				80				85				90			

acg gaa acc cac tat ctg caa gac ggt act gat gtc tcc ctc gct cga
 636

Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	Val	Ser	Leu	Ala	Arg
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 684

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 732

Gly	Tyr	Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg
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 780

Gly	Leu	Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	Leu	Glu	Pro	Met	Lys
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 828

Ser	Ala	Thr	Asn	Arg	Tyr	Lys	Leu	Phe	Pro	Ala	Lys	Lys	Leu	Lys	Ser
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 Lys Asn Val Phe Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys
 195 200 205

 aga gag acc ctc aag gca act aag tat gtg gag ctg gtg atc gtg gca
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 Arg Glu Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala
 210 215 220

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 Ala Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met
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 320 325 330

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 Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly
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 385 390 395

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 1644
 Phe Val Glu Glu Gly Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys
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 1740
 Val Cys Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala
 465 470 475

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 1788
 Gly Thr Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe
 480 485 490

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 1836
 Cys Thr Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp
 495 500 505 510

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 Gly His Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys
 515 520 525

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 1932
 Gln Thr His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys
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 1980
 Pro Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro
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 Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser
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 Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro
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 Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys
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 Asn Asn Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe
 675 680 685

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 690 695 700

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 2460
 Gln Ala Asp Asn Gln Gly Leu Thr Ile Gly Ile Leu Val Thr Ile Leu
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 Ile Arg Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg
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755 760 765

cac ctc ggc cac ctt gga aaa ggc ctg atg agg aag ccg cca gat tcc
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His Leu Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser
770 775 780

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Tyr Pro Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val
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Gly Thr Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro
850 855 860

ctg gcc aga aca act ccg ctc act cat gcc ttg gcc agg acc cca gga
2940
Leu Ala Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly
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2988
Gln Trp Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln
880 885 890

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3036
Tyr Pro His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys
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cgtagatatt 4176

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caacagttt 4596

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cagaaaacaa 4656

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attcatgact 4716

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ctaatacatt 4776

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aaatgtaaag 4836

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attacacttg 4896

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attttatggt 4956

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35 40 45

Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His
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Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
65 70 75 80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
85 90 95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
100 105 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr
115 120 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu
130 135 140

Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala
145 150 155 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg
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Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn
180 185 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu
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Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn
210 215 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg
225 230 235 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn
245 250 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys
260 265 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln
290 295 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro
305 310 315 320

Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp
325 330 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu
340 345 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser
355 360 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr
370 375 380

Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu
385 390 395 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro
405 410 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val
420 425 430

Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn
435 440 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys
450 455 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr
465 470 475 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr
485 490 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His
500 505 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala
530 535 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly
545 550 555 560

Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg
565 570 575

Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro
580 585 590

Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln
595 600 605

Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp
610 615 620

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Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly
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Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp
675 680 685

Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala
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705 710 715 720

Leu Ala Ala Gly Phe Val Val Tyr Leu Lys Arg Lys Thr Leu Ile Arg
725 730 735

Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val
740 745 750

Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu
755 760 765

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro
770 775 780

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile
785 790 795 800

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln

805

810

815

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820 825 830

Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr
835 840 845

Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala
850 855 860

Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp
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His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys
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cggggggaaa 120

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cgcgaggcgt 180

cgggagctga ctcgccgagg cagggaaatcc ctccggtcgc gacgccccggc
cccgctcggc 240

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 ctgaaggccc 300

gcgacg atg gca gcg cgc ccg ctg ccc gtg tcc ccc gcc cgc gcc ctc
 348

Met	Ala	Ala	Arg	Pro	Leu	Pro	Val	Ser	Pro	Ala	Arg	Ala	Leu
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 396

Leu	Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
15				20					25				30		

gtg agc tta tgg aac gaa gga aga gct gat gaa gtt gtc agt gcc tct
 444

Val	Ser	Leu	Trp	Asn	Glu	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	Ser
				35				40					45		

gtt cgg agt ggg gac ctc tgg atc cca gtg aag agc ttc gac tcc aag
 492

Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	Ser	Lys
				50			55			60					

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 540

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				65			70			75					

ctg atc ata aat ctg gaa aga aat gaa ggt ctc att gcc agc agt ttc
 588

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			80		85					90					

acg gaa acc cac tat ctg caa gac ggt act gat gtc tcc ctc gct cga
 636

Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	Val	Ser	Leu	Ala	Arg
			95		100				105				110		

aat tac acg gta att ctg ggt cac tgt tac tac cat gga cat gta cgg
 684

Asn	Tyr	Thr	Val	Ile	Leu	Gly	His	Cys	Tyr	Tyr	His	Gly	His	Val	Arg
				115			120			125					

gga tat tct gat tca gca gtc agt ctc agc acg tgt tct ggt ctc agg
 732

Gly	Tyr	Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg
				130			135			140					

gga ctt att gtg ttt gaa aat gaa agc tat gtc tta gaa cca atg aaa
 780

Gly	Leu	Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	Leu	Glu	Pro	Met	Lys
			145		150					155					

agt gca acc aac aga tac aaa ctc ttc cca gcg aag aag ctg aaa agc
 828

Ser	Ala	Thr	Asn	Arg	Tyr	Lys	Leu	Phe	Pro	Ala	Lys	Lys	Leu	Lys	Ser
			160		165					170					

gtc cgg gga tca tgt gga tca cat cac aac aca cca aac ctc gct gca
 876

Val	Arg	Gly	Ser	Cys	Gly	Ser	His	His	Asn	Thr	Pro	Asn	Leu	Ala	Ala

175	180	185	190
aag aat gtg ttt cca cca ccc tct cag aca tgg gca aga agg cat aaa 924			
Lys Asn Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys 195 200 205			
aga gag acc ctc aag gca act aag tat gtg gag ctg gtg atc gtg gca 972			
Arg Glu Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala 210 215 220			
gac aac cga gag ttt cag agg caa gga aaa gat ctg gaa aaa gtt aag 1020			
Asp Asn Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys 225 230 235			
cag cga tta ata gag att gct aat cac gtt gac aag ttt tac aga cca 1068			
Gln Arg Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro 240 245 250			
ctg aac att cgg atc gtg ttg gta ggc gtg gaa gtg tgg aat gac atg 1116			
Leu Asn Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met 255 260 265 270			
gac aaa tgc tct gta agt cag gac cca ttc acc agc ctc cat gaa ttt 1164			
Asp Lys Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe 275 280 285			
ctg gac tgg agg aag atg aag ctt cta cct cgc aaa tcc cat gac aat 1212			
Leu Asp Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn 290 295 300			
gcg cag ctt gtc agt ggg gtt tat ttc caa ggg acc acc atc ggc atg 1260			
Ala Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met 305 310 315			
gcc cca atc atg agc atg tgc acg gca gac cag tct ggg gga att gtc 1308			
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val 320 325 330			
atg gac cat tca gac aat ccc ctt ggt gca gcc gtg acc ctg gca cat 1356			
Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His 335 340 345 350			
gag ctg ggc cac aat ttc ggg atg aat cat gac aca ctg gac agg ggc 1404			
Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly 355 360 365			
tgt agc tgt caa atg gcg gtt gag aaa gga ggc tgc atc atg aac gct 1452			
Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala 370 375 380			

tcc acc ggg tac cca ttt ccc atg gtg ttc agc agt tgc agc agg aag
 1500
 Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys
 385 390 395

 gac ttg gag acc agc ctg gag aaa gga atg ggg gtg tgc ctg ttt aac
 1548
 Asp Leu Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn
 400 405 410

 ctg ccg gaa gtc agg gag tct ttc ggg ggc cag aag tgt ggg aac aga
 1596
 Leu Pro Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg
 415 420 425 430

 ttt gtg gaa gaa gga gag gag tgt gac tgt ggg gag cca gag gaa tgt
 1644
 Phe Val Glu Glu Gly Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys
 435 440 445

 atg aat cgc tgc tgc aat gcc acc acc tgt acc ctg aag ccg gac gct
 1692
 Met Asn Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala
 450 455 460

 gtg tgc gca cat ggg ctg tgc tgt gaa gac tgc cag ctg aag cct gca
 1740
 Val Cys Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala
 465 470 475

 gga aca gcg tgc agg gac tcc agc aac tcc tgt gac ctc cca gag ttc
 1788
 Gly Thr Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe
 480 485 490

 tgc aca ggg gcc agc cct cac tgc cca gcc aac gtg tac ctg cac gat
 1836
 Cys Thr Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp
 495 500 505 510

 ggg cac tca tgt cag gat gtg gac ggc tac tgc tac aat ggc atc tgc
 1884
 Gly His Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys
 515 520 525

 cag act cac gag cag cag tgt gtc aca ctc tgg gga cca ggt gct aaa
 1932
 Gln Thr His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys
 530 535 540

 cct gcc cct ggg atc tgc ttt gag aga gtc aat tct gca ggt gat cct
 1980
 Pro Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro
 545 550 555

 tat ggc aac tgt ggc aaa gtc tcg aag agt tcc ttt gcc aaa tgc gag
 2028
 Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu
 560 565 570

atg aga gat gct aaa tgt gga aaa atc cag tgt caa gga ggt gcc agc
2076
Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser
575 580 585 590

cg^g cca gtc att ggt acc aat gcc gtt tcc ata gaa aca aac atc ccc
2124
Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro
595 600 605

ctg cag caa gga ggc cg^g att ctg tgc cg^g ggg acc cac gt^g tac ttg
2172
Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu
610 615 620

ggc gat gac atg ccg gac cca ggg ctt gt^g ctt gca ggc aca aag tgt
2220
Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys
625 630 635

gca gat gga aaa atc tgc ctg aat cgt caa tgt caa aat att agt gtc
2268
Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val
640 645 650

ttt ggg gtt cac gag tgt gca atg cag tgc cac ggc aga ggg gt^g tgc
2316
Phe Gly Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys
655 660 665 670

aac aac agg aag aac tgc cac tgc gag gcc cac tgg gca cct ccc ttc
2364
Asn Asn Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe
675 680 685

tgt gac aag ttt ggc ttt gga gga agc aca gac agc ggc ccc atc cg^g
2412
Cys Asp Lys Phe Gly Phe Gly Ser Thr Asp Ser Gly Pro Ile Arg
690 695 700

caa gca gaa gca agg cag gaa gct gca gag tcc aac agg gag cgc gg^c
2460
Gln Ala Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly
705 710 715

cag ggc cag gag ccc gt^g gga tcg cag gag cat ggc tct act gcc tca
2508
Gln Gly Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser
720 725 730

ctg aca ctc atc tga gccctccat gacatggaga ccgtgaccag tgctgctgca
2563
Leu Thr Leu Ile
735

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gaagtccagc 2683

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gttagcttc 2743

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accactctgg 2803

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tcactgagcc 2863

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gatatggctt 2983

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agaagaaggt 3103

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gcagtactca 3163

gg tttgaggg tttcagaaaa gccaggaaac ccacagagtc accaaccctt
cat ttaacaa 3223

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ctgcataaaaa atagagtgc tttgaaata aaaaaaaaaa aaaaa
3328

<210> 4

<211> 738

<212> PRT

<213> Homo sapiens

<400> 4

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Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly Val Ser
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Leu Trp Asn Glu Gly Arg Ala Asp Glu Val Val Ser Ala Ser Val Arg
35 40 45

Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His
50 55 60

Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
65 70 75 80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
85 90 95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
100 105 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr
115 120 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu
130 135 140

Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala
145 150 155 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg
165 170 175

Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn
180 185 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu
195 200 205

Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn
210 215 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg
225 230 235 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn
245 250 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys
260 265 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln
290 295 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro
305 310 315 320

Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp
325 330 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu
340 345 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser
355 360 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr
370 375 380

Gly Tyr Pro Phé Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu
385 390 395 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro
405 410 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val
420 425 430

Glu Glu Gly Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn
435 440 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys
450 455 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr
465 470 475 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr
485 490 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His
500 505 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala
530 535 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly

545

550

555

560

Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg
565 570 575

Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Ala Ser Arg Pro
580 585 590

Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln
595 600 605

Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp
610 615 620

Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp
625 630 635 640

Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly
645 650 655

Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn
660 665 670

Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp
675 680 685

Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala
690 695 700

Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly
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Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr
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Leu Ile

<210> 5

<211> 2642

<212> DNA

<213> Homo sapiens

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agaagaccac 120

cattgaaaaa ctaagggtgtg tgccccccttc ccggccaccc cgtggcttcc
aaccctgtca 180

ggctcacctc ggccacccctg gaaaaggcct gatgaggaag ccgcacatt
cctacccacc 240

gaaggacaat cccagggat tgctgcagtgc tcagaatgtt gacatcagca
gaccctcaa 300

cggcctgaat gtccctcagc cccagtcaac tcagcgagtg ctccctcccc
tccaccggc 360

cccacgtgca cctagcgtcc ctgccagacc cctgccagcc aagcctgcac
ttaggcaggc 420

ccaggggacc tgtaagccaa acccccctca gaaggctctg cctgcagatc
ctctggccag 480

aacaactcgg ctcactcatg cttggccag gaccggagga caatgggaga
ctggcctcg 540

cctggcaccc ctcagacctg ctccacaata tccacaccaa gtgccagat
ccacccacac 600

cgccttatatt aagtgagaag ccgacaccc ttcaacag tgaagacaga
agttgcact 660

atcttcagc tccagttgga gtttttgta ccaactttta ggatttttt
taatgttaa 720

aacatcatta ctataagaac tttagctac tgccgtcagt gctgtgtgt
gctatggc 780

tctgtctact tgcacaggta ctgtaaatt attaatttat gcagaatgtt
gattacagt 840

cagtgcgtg tagtaggcat tttagccatc actgagttt ccatggcagg
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gtgcttttag tattttagtg aacttgaaat atcctgcttg atgggattct
ggacaggatg 960

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ccagctgtgc 1020

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ctgaccagcc 1320

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atcaacttcc 1920

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ttcaaatgcc 1980

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gaaatacaaa 2040

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tttcacatta 2100

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2642

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<211> 205

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val
35 40 45

Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu
50 55 60

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro
65 70 75 80

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile
85 90 95

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln
100 105 110

Arg Val Leu Pro Pro Leu His Arg Ala Pro Arg Ala Pro Ser Val Pro
115 120 125

Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr

130

135

140

Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala
145 150 155 160

Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp
165 170 175

Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln Tyr Pro
180 185 190

His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys
195 200 205

<210> 7

<211> 908

<212> DNA

<213> Homo sapiens

<400> 7

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catgacatgg 120

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ctgtgactgg 180

cagcattgac tctgtggctt tgccatcggt tccatgacaa cagacacaac
acagttctcg 240

gggctcagga ggggaagtcc agcctaccag gcaggtctgc agaaacagtg
caaggaaggg 300

cagcgacttc ctggttgagc ttctgctaaa acatggacat gttcagtgc
tgctcctgag 360

agagtagcag gttaccactc tggcaggccc cagccctgca gcaaggagga
agaggactca 420

aaagtctggc ctttcaactga gcctccacag cagtggggga gaagcaaggg
ttggggccag 480

tgtccccctt ccccagtgac acctccgcct tggcagccct gatgactgg
ctctggctgc 540

aacttaatgc tctgatatgg ctttttagcat ttatttatag aaaatagcag
gttttagtt 600

ttaatttat cagagaccct gccacccatt ccatctccat ccaagcaaac
tgaatggcat 660

tgaaacaaac tggagaagaa ggtaggagaa agggcggtga actctggctc
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acatgcgtga ccagcagtac tcaggttga gggttgcag aaagccaggg
aaccacaga 780

gtcaccaacc cttcatttaa caagtaagaa tgtaaaaaag tgaaaacaat
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aaaaaaaaa
908

<210> 8

<211> 34

<212> PRT

<213> Homo sapiens

<400> 8

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20 25 30

Leu Ile

<210> 9

<211> 23

<212> DNA

<213> Homo sapiens

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23

<210> 10

<211> 23

<212> DNA

<213> Homo sapiens

<400> 10
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23

<210> 11

<211> 24

<212> DNA

<213> Homo sapiens

<400> 11
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24

<210> 12

<211> 24

<212> DNA

<213> Homo sapiens

<400> 12
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24

<210> 13

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (15)..(15)

<223> Mismatch (g instead of c)

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23

<210> 14
<211> 23
<212> DNA
<213> Homo sapiens

<400> 14
ggactctgca gcttcctgcc ttg
23

<210> 15
<211> 21
<212> DNA
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<400> 15
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21

<210> 16
<211> 21
<212> DNA
<213> Homo sapiens

<400> 16
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21

<210> 17
<211> 24
<212> DNA
<213> Homo sapiens

<400> 17
ggccgggtga tctttgggtct cttc
24

<210> 18
<211> 24
<212> DNA
<213> Homo sapiens

<400> 18
cccggtgtc tgtcttggtg ctct
24

<210> 19
<211> 21
<212> DNA
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<400> 19
ctgctgagat gggaaagggc t
21

<210> 20
<211> 21
<212> DNA
<213> Homo sapiens

<400> 20
ttcaggataa tcacacctgagc a
21